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Conference Abstract

The Taxonomic and Biodiversity Software Stack in R

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Abstract

High quality R software for taxonomy and biodiversity occurrence data are important, both
because there are a large number of biologists who use R, and because R allows
reproducible and open science. I will do an overview of the software that our non-profit
organization rOpenSci (https://ropensci.org) produces for both taxonomy and biodiversity
work, their use cases, and future improvements. In addition, I will provide details about our
latest work on software that defines taxonomic classes for consistent and powerful
manipulations of taxonomic data (for example, select certain taxonomic names, and
associated data are selected for those taxa). Finally, I will discuss new R software (pegax (
https://github.com/ropenscilabs/pegax)) for high performance taxonomic name parsing,
which will allow fast and operating system independent parsing of taxonomic names.

Keywords

taxonomy, software, R, rstats

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